IN THE CLAIMS:

Please amend claims 1, 4-10, 12, 16, 20, 23-25, 30, 34, 36-37, 40, 42-44, and 47-48. Cancel claims 11 and 35 as follows. For the Examiner's convenience, all pending claims are reproduced below. Applicant adds new claims 49-52.

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1 (Amended). A computer-implemented method of presenting expression level information as collected from first and second samples, said method comprising **[the steps of]**:

displaying a first axis **[corresponding to]** indicating expression level in said first sample;

displaying a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating expression level in said second sample; **[and]**

for a selected expressed sequence, displaying a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to said first axis and said Y coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with an expression level of said selected expressed sequence in said first sample and relative to said second axis in accordance with an expression level of said selected expressed sequence in said second sample;

receiving an input of a user's selection of said mark; and

in response to said user input, displaying information about said selected expressed sequence.

2. The method of claim 1 wherein said selected expressed sequence comprises a gene.

Duplicate claims

3. The method of claim 1 wherein said selected expressed sequence comprises a portion of a gene.

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4 (Amended). The method of claim 1 further comprising: **[the step of]**

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repeatedly **[repeating said]** displaying a mark **[step]** for each one of a plurality of selected expressed sequences.

5 (Amended). The method of claim 1 further comprising **[the steps of]**:

monitoring said expression level of said expressed sequence in said first sample and said second sample.

6 (Amended). The method of claim **[3]** 5 wherein said monitoring **[step for one of said samples]** further comprises **[substeps of]**:

inputting a plurality of hybridization intensities **[of]** from pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples;

comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and

generating said expression level for said expressed sequence and said one of said samples responsive to results of said comparing **[step]**.

7 (Amended). The method of claim 6 further comprising **[the step of]**:

comparing a difference between hybridization intensities of perfect match and mismatch probes at a base position to a difference threshold.

8 (Amended). The method of claim 7 further comprising **[the step of]**:

comparing a quotient of hybridization intensities of perfect match and mismatch probes at a base position to a ratio threshold.

9 (Amended). The method of claim 6 further comprising **[the steps of]**:

a) counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a

difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

b) counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold; **[and]**

c) computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity; and

d) computing a difference of said perfect match probe intensity to said mismatch probe intensity.

10 (Amended). The method of claim 9 further comprising **[the steps of]**:

repeating said a), b), c) and **[c)]** d) steps for each of said probe pairs, accumulating a sum of differences of said perfect match and mismatch probe intensities for probe pairs that **[cause]** exhibit said difference; and

determining an expression level of said selected expressed sequence to be an average of said differences.

11. Canceled.

11 12 (Amended). The method of claim 1 **[11]** further comprising **[the steps of]**:

in response to said **[user]** input, displaying information about said selected expressed sequence; said information comprising an identifier for said selected expressed sequence.

12 13 (Amended). The method of claim 11 12 wherein said **[information about]** identifier for said selected expressed sequence comprises a GenBank accession number.

14. The method of claim 12 wherein said information about said selected expressed sequence comprises a GenBank database record for said selected expressed sequence.

15. The method of claim 1 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

15 16 (Amended). The method of claim 14 wherein said particular characteristic comprises **[presence of]** a disease state.

17. The method of claim 15 wherein said particular characteristic comprises a treatment strategy for a disease.

18. The method of claim 1 wherein said particular characteristic is a stage of a disease.

18 19 (Amended). The method of claim 1 further comprising **[the step of]** :

displaying a third axis substantially perpendicular to said first axis and to said second axis in a three-dimensional display environment wherein said position of said mark is further selected relative to said third axis in accordance with an expression level of said selected expressed sequence in a third sample.

19 20 (Amended). A computer-implemented method of presenting sample analysis information comprising **[the steps of]**:

displaying a first axis **[corresponding to]** indicating a concentration of a compound in a first sample as determined by monitoring binding of said compound to a selected polymer having binding affinity to said compound;

displaying a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating a concentration of said compound in said second sample as determined by monitoring binding of said compound to said selected polymer; and

displaying a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to said first axis and said Y

coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample;

receiving an input of a user's selection of said mark; and

in response to said user input, displaying information about said ~~selected~~ compound ~~expressed sequence~~.

21. The method of claim 20 wherein said selected polymer comprises a nucleic acid sequence.

22. The method of claim 20 wherein said selected polymer comprises a protein.

22 ~~23~~ (Amended). The method of claim ~~21~~ 20 further comprising **[the step of]**: obtaining said concentration of said compound in said first sample by exposing said first sample to a plurality of nucleic acid probes.

23 ~~24~~ (Amended). The method of claim ~~22~~ 21 further comprising **[the step of]**: obtaining said concentration of said compound in said first sample by exposing said first sample to a plurality of peptide probes.

24 ~~25~~ (Amended). A computer program product for presenting expression level information as collected from a first sample and a second **[samples]** sample, said product comprising:**[:]**

code for displaying a first axis **[corresponding to]** indicating expression level in said first sample;

code for displaying a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating expression level in said second sample;

code for, for a selected expressed sequence, displaying a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to said first axis and said Y coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with an

expression level of said selected expressed sequence in said first sample and relative to said second axis in accordance with an expression level of said selected expressed sequence in said second sample;

code for receiving an input from a user's selection of said mark;

code for displaying information about said selected expressed sequence in response to said user input; and

a computer-readable storage medium for storing the codes.

26. The product of claim 25 wherein said selected expressed sequence comprises a gene.

27. The product of claim 25 wherein said selected expressed sequence comprises a portion of a gene.

28. The product of claim 25 further comprising code for repeatedly applying said displaying a mark code for a plurality of selected expressed sequences.

29. The product of claim 25 further comprising:

code for monitoring said expression level of said expressed sequence in said first sample and said second sample.

~~29~~ 30 (Amended). The product of claim **[27]** ~~29~~ 28 wherein said code for monitoring **[step]** for one of said samples comprises:

code for inputting a plurality of hybridization intensities **[of]** from pairs of perfect match and mismatch probes, said perfect match probes being perfectly complementary to a target nucleic acid sequence indicative of expression of said selected gene and said mismatch probes having at least one base mismatch with said target sequence, and said hybridization intensities indicating hybridization affinity between said perfect match and mismatch probes and a sample nucleic acid sequence from said one of said samples;

code for comparing the hybridization intensities of each pair of perfect match probe and mismatch probe; and

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code for generating said expression level for said expressed sequence and said one of said samples responsive to a result produced by **[results of]**said code for comparing **[step]**.

31. The product of claim 30 further comprising:

code for comparing a difference between hybridization intensities of perfect match and mismatch probes at a base position to a difference threshold.

32. The product of claim 31 further comprising:

code for comparing a quotient of hybridization intensities of perfect match and mismatch probes at a base position to a ratio threshold.

Duplicate claim

33. The product of claim 30 further comprising:

a) code for counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

b) code for counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold; and

c) code for computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity.

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33 ~~34~~ 32 (Amended). The product of claim ~~33~~ further comprising:

code for repeatedly applying said a), b), and c) codes for each of said probe pairs, accumulating a sum of differences of said perfect match and mismatch probe intensities for probe pairs that **[cause]** exhibit said difference; and

code for determining an expression level of said selected expressed sequence to be an average of said differences.

35. Canceled.

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34 ~~36~~ (Amended). The product of claim **[35]** ~~25~~ 24 further comprising:
code for, in response to said **[user]** input, displaying information about said selected expressed sequence; said information comprising an identifier for said selected expressed sequence.

~~35~~ 37 (Amended). The product of claim ~~36~~ 34 wherein said **[information about]** identifier for said selected expressed sequence comprises a GenBank accession number.

38. The product of claim 36 wherein said information about said selected expressed sequence comprises a GenBank database record for said selected expressed sequence.

39. The product of claim 25 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

Dupl. cate claim

~~38~~ 40 (Amended). The product of claim ~~39~~ 37 wherein said particular characteristic comprises **[presence of]** a disease state.

~~39~~ 41. The product of claim ~~39~~ wherein said particular characteristic comprises a treatment strategy for a disease.

Duplicate claim

~~40~~ 42 (Amended). The product of claim **[25]** ~~39~~ 37 wherein said particular characteristic is a stage of a disease.

~~41~~ 43 (Amended). The product of claim ~~25~~ 24 further comprising **[the step of]** :
code for displaying a third axis substantially perpendicular to said first axis and to said second axis in a three-dimensional display environment wherein said position of said mark is further selected relative to said third axis in accordance with an expression level of said selected expressed sequence in a third sample.

~~42~~ 44. A computer program product for presenting sample analysis information comprising:

code for displaying a first axis **[corresponding to]** indicating a concentration of a compound in a first sample as determined by monitoring binding of said compound to a selected polymer having bonding affinity to said compound;

code for displaying a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating a concentration of said compound in a second sample as determined by monitoring binding of said compound to said selected polymer;

code for displaying a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to said first axis and said Y coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample; **[and]**

code for receiving an input of a user's selection of said mark;

code for displaying information about said ~~selected expressed sequence~~ compound in response to said user input; and

a computer-readable storage medium that stores the codes.

45. The product of claim 44 wherein said selected polymer comprises a nucleic acid sequence.

46. The product of claim 44 wherein said selected polymer comprises a protein.

45 47 (Amended). A computer system comprising a display, a processor, and a memory that stores instructions for configuring said processor to:

display a first axis **[corresponding to]** indicating expression level in said first sample;

display a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating expression level in said second sample; and

for a selected expressed sequence, display a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to

said first axis and said Y coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with an expression level of said selected expressed sequence in said first sample and relative to said second axis in accordance with an expression level of said selected expressed sequence in said second sample; wherein information about said selected expressed sequence is displayed responsive to an input of a user's selection of said mark.

Cl 13 Conclude

46 ~~48~~. (Amended). A computer system comprising a display, a processor, and a memory that stores instructions for configuring said processor to:

display a first axis **[corresponding to]** indicating a concentration of a compound in a first sample as determined by monitoring binding of said compound to a selected polymer having binding affinity to said compound;

display a second axis substantially perpendicular to said first axis, said second axis **[corresponding to]** indicating a concentration of said compound in said second sample as determined by monitoring binding of said compound to said selected polymer; and

display a mark at a position with an X coordinate and a Y coordinate, wherein the X coordinate of said position is selected relative to said first axis and said Y coordinate of said position is selected relative to said second axis, wherein said position is selected relative to said first axis in accordance with said concentration in said first sample and relative to said second axis in accordance with said concentration in said second sample; wherein information about said selected expressed sequence is displayed responsive to an input of a user's selection of said mark.

Cl 14

47 ~~49~~. (New) The method of claim 1 further comprising:

providing a tactile feedback to said user through a pointing device when a cursor is moved over said mark; said tactile feedback indicating expression level for said selected expressed sequence corresponding to said mark.

48 ~~50~~. (New) The method of claim 1 further comprising:

providing an aural indication to said user through a pointing device when a cursor is moved over said mark; said aural indication indicating expression level for said selected expressed sequence corresponding to said mark.

49 51. (New) The method of claim 1 further comprising:

obtaining information from an internet based resource about a selected expressed sequence corresponding to said mark.

50 52. (New) The method of claim 1 further comprising:

receiving from the user a selection of at least two of a plurality of marks, said marks;

displaying information about genes corresponding to said selection of at least two of a plurality of marks.

REMARKS

REJECTIONS UNDER 35 U.S.C. § 112(2)

Applicant amends the claims to avoid the Examiner's 35 U.S.C. 112 rejections in paragraphs A-P. No amendment should be construed as acquiescence in any grounds of rejection.

Regarding the Examiner's rejection in paragraph A, applicant notes that the axes that define a coordinate system meet at a point called the "origin" and are thus connected. However, applicant notes that not all embodiments according to the present invention need necessarily display the origin, or connection point, of the axes. Applicant believes the issue is not one of indefiniteness, but rather one of scope, and has therefore not changed the claims.

Regarding the Examiner's rejection in paragraph N, applicant notes the specification describes the treatment strategy as a characteristic on page 12, lines 22-25:

> One can compare expression levels among tissue samples at successive stages or severity levels of the same disease, among tissue samples where different ultimate outcomes of the disease (e.g., patient death or